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OM nucleic - nucleic search, using sw model

Run on: November 5, 2004, 19:26:33 ; Search time 87 Seconds
(without alignments)
4027.804 Million cell updates/sec

Title: US-09-882-434A-2
Perfect score: 493
Sequence: 1 attaatgtcttgatgtctcat.....ccatgtgatgttttacc 493

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 35539441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	34.8	7.1	179	US-09-382-552-43	Sequence 43, Appl
C 2	34	6.9	337	US-09-270-767-29138	Sequence 29138, A
C 3	34	6.9	1133	US-09-270-767-13217	Sequence 13217, A
C 4	33.4	6.8	9223	US-08-961-527-59	Sequence 59, Appl
C 5	33	6.7	62909	US-09-596-002-32	Sequence 32, Appl
C 6	32.4	6.6	972	US-09-248-796A-13663	Sequence 13663, A
C 7	32.2	6.5	1137	US-09-248-796A-4423	Sequence 4423, Ap
C 8	32.2	6.5	1422	US-09-134-001C-1936	Sequence 1936, Ap
C 9	32	6.5	291	US-09-540-236-398	Sequence 398, Ap
C 10	32	6.5	92407	US-09-596-002-36	Sequence 36, Appl
C 11	32	6.5	202001	US-09-734-674-3	Sequence 3, Appl
C 12	31.8	6.5	537	US-08-845-539-5	Sequence 5, Appl
C 13	31.8	6.5	537	US-09-362-642-5	Sequence 5, Appl
C 14	31.6	6.4	6354	US-09-058-389A-5	Sequence 5, Appl
C 15	31.6	6.4	6354	US-09-611-781-5	Sequence 5, Appl
C 16	31.6	6.4	1664976	US-08-916-421B-1	Sequence 1, Appl
C 17	31.6	6.4	1664976	US-09-692-570-1	Sequence 1, Appl
C 18	31.4	6.4	561	US-09-540-236-1317	Sequence 1317, Ap
C 19	31.4	6.4	3189	US-09-710-279-3694	Sequence 3694, Ap
C 20	31.4	6.4	3223	US-09-710-279-4222	Sequence 4222, Ap
C 21	31.4	6.4	246240	US-08-724-394A-20	Sequence 20, Appl
C 22	31.4	6.4	246240	US-08-724-394A-21	Sequence 21, Appl
C 23	31.4	6.4	246240	US-08-724-394A-22	Sequence 22, Appl
C 24	31.4	6.4	1664976	US-08-916-421B-1	Sequence 1, Appl
C 25	31.4	6.4	1664976	US-09-692-570-1	Sequence 1, Appl
C 26	31.2	6.3	4417	US-07-741-453A-57	Sequence 57, Appl
C 27	31.2	6.3	5915	US-09-382-552-3	Sequence 3, Appl

C 28	31.2	6.3	6240	4	US-09-382-552-117	Sequence 117, Appl
C 29	31.2	6.3	6909	4	US-09-382-552-21	Sequence 21, Appl
C 30	31.2	6.3	6910	4	US-09-382-552-15	Sequence 15, Appl
C 31	31.2	6.3	6911	4	US-09-382-552-1	Sequence 1, Appl
C 32	31.2	6.3	6911	4	US-09-382-552-14	Sequence 14, Appl
C 33	31.2	6.3	6911	4	US-09-382-552-16	Sequence 16, Appl
C 34	31.2	6.3	6911	4	US-09-382-552-17	Sequence 17, Appl
C 35	31.2	6.3	6911	4	US-09-382-552-18	Sequence 18, Appl
C 36	31.2	6.3	6911	4	US-09-382-552-19	Sequence 19, Appl
C 37	31.2	6.3	6911	4	US-09-382-552-20	Sequence 20, Appl
C 38	31.2	6.3	6912	4	US-09-382-552-13	Sequence 13, Appl
C 39	31	6.3	4301	3	US-08-121-446-3	Sequence 3, Appl
C 40	31	6.3	112132	4	US-09-741-150-3	Sequence 3, Appl
C 41	31	6.3	112132	4	US-10-160-187-3	Sequence 3, Appl
C 42	30.8	6.2	444	4	US-09-248-796A-3435	Sequence 3435, Ap
C 43	30.8	6.2	3715	3	US-09-600-776-9	Sequence 9, Appl
C 44	30.6	6.2	1569	4	US-09-248-796A-2847	Sequence 2847, Ap
C 45	30.6	6.2	5361	3	US-08-973-462-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-382-552-43/c
; Sequence 43, Application US/09382552
; Patent No. 6673909

GENERAL INFORMATION:
; APPLICANT: Brown, Jr., Robert H.
; APPLICANT: Liu, Jing
; APPLICANT: Aoki, Masashi
; APPLICANT: Ho, Meng
; APPLICANT: Matsuda-Asada, Chie
; TITLE OF INVENTION: DYSPERLIN, A GENE MUTATED IN DISTAL MYOPATHY AND LIMB
; FILE REFERENCE: 00786/399002
; CURRENT APPLICATION NUMBER: US/09/382,552
; CURRENT FILING DATE: 1999-08-25
; EARLIER APPLICATION NUMBER: US 60/097,927
; EARLIER FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 179
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-382-552-43

Query Match	7.1%	Score 34.8	DB 4	Length 179
Best Local Similarity	65.4%	Pred. No. 0.11		
Matches	51	Conservative	0	Mismatches 27; Indels 0; Gaps 0
QY	22	CATACCTCTTCCTCCCACTTATCAGTAACTCAGCTAGCCATGCGCTTCACC	81	
Db	155	CCTGCTCCTCTGCTCTTACCATTTTCCCGCAAGTGCCTCCCAAGGGGTCCACC	96	
QY	82	AGTTGTTCTTCTCAGTC	99	
Db	95	AGTTTCTTCTTGTACTC	78	

RESULT 2
US-09-270-767-29138
; Sequence 29138, Application US/09270767
; Patent No. 6703491
GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7328-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0

```
; SEQ ID NO 29138
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-29138

Query Match
Best Local Similarity 6.9%; Score 34; DB 4; Length 337;
Matches 82; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 329 CCAGGCGATGCAACCTTTTGGTTGGAGAGATATCTTCATCCAACTGCTAGATTCATTAAC 388
Db 13 CAAGGGGCACTCCGCTTTTGGTTGGTTATCAATGCTAGCCATTGAATATATATAT 72

QY 389 TCTTGGATCCATCTTCTATGTTTTCAGTGTATATTAATAGAGATGCTGATATATAA 448
Db 73 ATTATCAATTTTCATTACATTAATCACTTATATATCAACATATGATTAATGAAATTGG 132

QY 449 TAAATAAGTAAAGCTACGGTATCACCATGCTGATGATTTTAA 490
Db 133 TACAGTCTGAAATATGCGTTTATACGAACGATATTTTAA 174

RESULT 3
US-09-270-767-13217
; Sequence 13217, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13217
; LENGTH: 1133
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13217

Query Match
Best Local Similarity 6.9%; Score 34; DB 4; Length 1133;
Matches 82; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 329 CCAGGCGATGCAACCTTTTGGTTGGAGAGATATCTTCATCCAACTGCTAGATTCATTAAC 388
Db 13 CAAGGGGCACTCCGCTTTTGGTTGGTTATCAATGCTAGCCATTGAATATATATAT 72

QY 389 TCTTGGATCCATCTTCTATGTTTTCAGTGTATATTAATAGAGATGCTGATATATAA 448
Db 73 ATTATCAATTTTCATTACATTAATCACTTATATATCAACATATGATTAATGAAATTGG 132

QY 449 TAAATAAGTAAAGCTACGGTATCACCATGCTGATGATTTTAA 490
Db 133 TACAGTCTGAAATATGCGTTTATACGAACGATATTTTAA 174

RESULT 4
US-08-961-527-59/c
; Sequence 59, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 351
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 9223 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-59

Query Match
Best Local Similarity 6.8%; Score 33.4; DB 4; Length 9223;
Matches 70; Conservative 1; Mismatches 62; Indels 0; Gaps 0;

QY 360 TATCTTCATCCAACTGCTAGATTCATTAATCACTTGGATCCATCTTCTATGTTTCAAGTG 419
Db 4971 TATTTTCAAAAATATATCATATAGTTTCATCTTCAGTAATTTTCTATATTTTCGTTGCAG 4912

QY 420 TATAATTAGAGATGCTGATATATAATAAAGTAAAGCTACGGTATCACCATCT 479
Db 4911 TCCAAATTAGAAATAGCTTGTAACTAATAGAAACAGGTGTATGCAATGAATTAAGTCT 4852

QY 480 GATGATTTTACC 492
Db 4851 TGTGAAAGCTACC 4839

RESULT 5
US-09-596-002-32/c
; Sequence 32, Application US/09596002
; Patent No. 6632636
; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert, E.
; APPLICANT: Patterson, Chandra
; APPLICANT: Berg, Kim, L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
; FILE REFERENCE: PM-0008-4 US
; CURRENT APPLICATION NUMBER: US/09/596,002
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/140,121
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PERL Program
; SEQ ID NO 32
; LENGTH: 62909
; TYPE: DNA
; ORGANISM: M. catarrhalis
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte template ID No. 6632636 32
; PUBLICATION INFORMATION:
US-09-596-002-32

Query Match
Best Local Similarity 6.7%; Score 33; DB 4; Length 62909;
Matches 69; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
```

US-09-248-796A-4423

Query Match 6.5%; Score 32.2; DB 4; Length 1137;
Best Local Similarity 56.0%; Pred. No. 2.3;
Matches 61; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 327 TGCAGGGCATGCAACCCCTTTGGTTGGAGAGTATCTTCATCCAAATGCTAGATTTTCA 386
Db 57540 TGCACAGAAATGGAGCTTACGGGTTCATCTATCTCTGCCCAGTGTGATTTGAT 57481

QY 387 ACTCTTGGATCCATCTTCTATGTTTTCAGTGTATATAATPAGAGAGATGCATGATAT 446
Db 57480 AATTTTGCATAAATCTGTAGATTGCTCTTGGCTGAGTGCATGAACCTTGGTTGGATATTT 57421

QY 447 AATAAATAA 455
Db 57420 GATCCAAA 57412

RESULT 6
US-09-248-796A-13663/c
; Sequence 13663, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 13663
; LENGTH: 972
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-13663

Query Match 6.6%; Score 32.4; DB 4; Length 972;
Best Local Similarity 48.9%; Pred. No. 1.8;
Matches 87; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 288 TGGATGACAGTGGTGTGACACACAGAGTTTGGGTCCAGTGCAGGGGATGCAACCCCTTT 347
Db 751 TTGATTCAGTGGTGTGACACACAGAGTTTGGGTCCAGTGCAGGGGATGCAACCCCTTT 692

QY 348 TGGTGGAGAGTATCTTCATCCATGCTAGATTTTCAATCTTGGATCCATCTTCTAT 407
Db 691 TACCAGTACGAGTGGATTCACCAATGATTAAGTAGACACACTGATAGTCCAGTAAT 632

QY 408 GTTTTTCAGTGTATATAATTAGAGAGATGATGATATATAATAAATAAGTAAAGCTA 465
Db 631 TTGATTCATAGTTGGAATTGATTTGCTAGTATTCAGCTTTTAAAGATGAACCTATA 574

RESULT 7
US-09-248-796A-4423/c
; Sequence 4423, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 4423
; LENGTH: 1137
; TYPE: DNA
; ORGANISM: Candida albicans

US-09-134-001C-1936/c

Query Match 6.5%; Score 32.2; DB 3; Length 1422;
Best Local Similarity 57.4%; Pred. No. 2.6;
Matches 58; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 371 AATGCTAGATTTTCATTAATTAATAAATAAGTAAAGCTACGGTAT 471
Db 1232 AATTTCTTTTGGTTTAAATCTTCAATATATTGTGGAGATTTAAATCAATTAATTTCTTT 1173

QY 431 AGATGCTAGTATATATAATAAATAAGTAAAGCTACGGTAT 471
Db 1172 AGATACAAATATAATAATAAATAAGTAAAGCTACGGTAT 1132

RESULT 8
US-09-134-001C-1936/c
; Sequence 1936, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1936
; LENGTH: 1422
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1936

Query Match 6.5%; Score 32.2; DB 3; Length 1422;
Best Local Similarity 57.4%; Pred. No. 2.6;
Matches 58; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 371 AATGCTAGATTTTCATTAATTAATAAATAAGTAAAGCTACGGTAT 471
Db 1232 AATTTCTTTTGGTTTAAATCTTCAATATATTGTGGAGATTTAAATCAATTAATTTCTTT 1173

QY 431 AGATGCTAGTATATATAATAAATAAGTAAAGCTACGGTAT 471
Db 1172 AGATACAAATATAATAATAAATAAGTAAAGCTACGGTAT 1132

RESULT 9
US-09-540-236-398/c
; Sequence 398, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATFA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 398
; LENGTH: 291
; TYPE: DNA
; ORGANISM: M. catarrhalis
US-09-540-236-398

Query Match 6.5%; Score 32; DB 4; Length 291;
Best Local Similarity 54.2%; Pred. No. 1.2;
Matches 65; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 363 CTTCATCCAAATGCTAGATTTCATACTCTTGGATCCATCTTCTATGTTTTTCAAGTGTAT 422

Db 159 CTCAGCCATCTCTGTTTTTATACAAACACGCACTTCAAGTTTTTGATCGCAGT 100
QY 423 AATTAGAGAGATGCGATGATATATAAATAGTAAAGCTACGGTATCACCATGTGAT 482
Db 99 TTTTGTGTGAATTTTGTATTATATCAAAACATTTAAGGCAAGGTATGCCCATATGAT 40

RESULT 10

US-09-596-002-36/c
; Sequence 36, Application US/09596002
; Patent No. 6632636
; GENERAL INFORMATION:

; APPLICANT: Lagace, Robert, E.

; APPLICANT: Patterson, Chandra

; APPLICANT: Berg, Kim, L.

; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME

; FILE REFERENCE: PM-0008-4 US

; CURRENT APPLICATION NUMBER: US/09/596,002

; CURRENT FILING DATE: 2000-06-16

; PRIOR APPLICATION NUMBER: 60/140,121

; PRIOR FILING DATE: 1999-06-18

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PERL Program

; SEQ ID NO 36

; LENGTH: 92407

; TYPE: DNA

; ORGANISM: M. catarrhalis

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte template ID No. 6632636 36

; PUBLICATION INFORMATION:

US-09-596-002-36

Query Match

Best Local Similarity 6.5%; Score 32; DB 4; Length 92407;

Matches 65; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 363 CTCATCAAGCTAGATTTCATACACTCTTGATCCATCTCTATGTTTTCAGTGTAT 422
Db 66073 CTCAGCCATCTCTGTTTTTATACAAACACGCACTTCAAGTTTGGATCGGAGT 66014
QY 423 AATTAGAGAGATGCGATGATATAATAAAGTAAAGCTACGGTATCACCATGTGAT 482
Db 66013 TTTTGTGTGAATTTTGTATTATATCAAAACATTTAAGGCAAGGTATGCCCATATGAT 65954

RESULT 11

US-09-734-674-3/c

; Sequence 3, Application US/09734674

; Patent No. 6498022

; GENERAL INFORMATION:

; APPLICANT: WEI, Ming-Hui et al

; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: CL001018

; CURRENT APPLICATION NUMBER: US/09/734,674

; CURRENT FILING DATE: 2000-12-13

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 202001

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(202001)

; OTHER INFORMATION: n = A,T,C or G

US-09-734-674-3

Query Match

Best Local Similarity 6.5%; Score 32; DB 4; Length 202001;

Matches 65; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Matches 59; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
QY 10 TTGAGTCTCATACATCTCTTCTCTCCCAACATTAGCACTTATCAGCTAACCTCAGCC 69
Db 150243 TTGAGTTGAATACTGATTCTGCCCTTTCTAGCTATTGATCTTAGCAATCACCACCC 150184
QY 70 ATGGCTTCCACCAAGTTGTTCTTCTCAGTCATCTACTGTGATCAT 113
Db 150183 CTGAGTTTCTATGAATTCATTATATAACTAATAATAATAATTAT 150140

RESULT 12

US-08-845-539-5

; Sequence 5, Application US/08845539

; Patent No. 5929303

; GENERAL INFORMATION:

; APPLICANT: Bennett, Alan B.

; APPLICANT: Rose, Jocelyn K.C.

; TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation

; TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/845,539

; FILING DATE: 25-APR-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Bastian, Kevin L.

; REGISTRATION NUMBER: 34,774

; REFERENCE/DOCKET NUMBER: 023070-0782000US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 537 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..537

; OTHER INFORMATION: /product= "melon CmEx1"

US-08-845-539-5

Query Match

Best Local Similarity 6.5%; Score 31.8; DB 2; Length 537;

Matches 69; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 238 GGCTATGACTTCAGTACACTGGACAACTGCTCTCTCTACACCGGCTGGATGCAGT 297
Db 82 GGCTATGGCGTCAACACAGCTGCTCTTAGTACTGCTTCTTCAACATGGCTGAGCTGT 141
QY 298 GGTCTTGCACACACAGGTTTGGTCCAGTCCAGGGGATCAACCCCTTTTGGTTGGAAG 357
Db 142 GGTGCTTGTGATGATCAAGTGTGCTAATGACCTCGATGCTGCTTCTTGGTAGCCCT 201
QY 358 AGTATCTTCAT 368
Db 202 TGTATCTTCAT 212

RESULT 13
US-09-362-642-5
; Sequence 5, Application US/09362642
; Patent No. 6350935
; GENERAL INFORMATION:
; APPLICANT: Bennett, Alan B.
; APPLICANT: Rose, Jocelyn K.C.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
; TITLE OF INVENTION: to Control Fruit Texture and Softening
; FILE REFERENCE: 023070-078210US
; CURRENT APPLICATION NUMBER: US/09/362,642
; CURRENT FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Cucumis melo
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(537)
; OTHER INFORMATION: melon expansin (CmEx1) partial cDNA clone
; US-09-362-642-5

Query Match 6.5%; Score 31.8; DB 3; Length 537;
Best Local Similarity 52.7%; Pred. No. 2;
Matches 69; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
QY 238 GGCTATGACTTCACTACATGCGCAAACTGCTCTCTCAACACGAGCTGGATGAGT 297
Db 82 GGCTATGGGTCACACAGCTGCTTTAGTACTGCTTTCTTCAACAATGGCCCTCAGCTGT 141
QY 298 GGTTTGACACACACAGCTTTGGTTCAGTCCAGGGCATCAACCTTTTGGTGAAG 357
Db 142 GGTGCTTGTGTGATCAAGTGTCTTAATGACCTCGATGCTGCTGCTGGTGGACCT 201
QY 358 AGTATCTTCAT 368
Db 202 TGTATCTTCAT 212

RESULT 14
US-09-058-389A-5
; Sequence 5, Application US/09058389A
; Patent No. 6130065
; GENERAL INFORMATION:
; APPLICANT: Belt, Judith A.
; APPLICANT: Crawford, Charles R.
; APPLICANT: Patel, Divyen
; TITLE OF INVENTION: A NITROBENZYLMECAPTOPURINERIBOSIDE
; TITLE OF INVENTION: (NEMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
; TITLE OF INVENTION: PROTEIN, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
; TITLE OF INVENTION: USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/058,389A
; FILING DATE: April 9, 1998
; CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-013N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6354 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; US-09-058-389A-5

Query Match 6.4%; Score 31.6; DB 3; Length 6354;
Best Local Similarity 46.4%; Pred. No. 9.4;
Matches 103; Conservative 0; Mismatches 119; Indels 0; Gaps 0;
QY 78 CACCAAGTTCTTCTTCAGTCATTACTGTGATGATCTCATAGCAATGGCAAGTGAGAT 137
Db 5639 CACCTGTCCGTCTTCCCGCCATCACAGCCATGTGACCAAGTCCACCAAGTCCCTGGAA 5698
QY 138 GGTGAATGGGAGTCCATTACAGTATGGAGTGTCCAGATTGTAAACACCGTGTCTGAGCG 197
Db 5699 GTGGAGTGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5758
QY 198 ATATAGCAAGTGTGGATGCTCAGCTATACATACAGAGGAGGAGGAGGAGGAGGAGGAGG 257
Db 5759 GGAGAGGGAGTGGAGACCAAGTATGAGCTGCAGCCGTTTCCCTCCCAAGGTCAGTTCT 5818
QY 258 TGGACAAACTGCTCTCTCTACACACGAGGCTGGATGAGTGG 299
Db 5819 AACCCTATCTGCTGCTTCTCTCTTCAACATCATGAGCTGG 5860

RESULT 15
US-09-611-781-5
; Sequence 5, Application US/09611781
; Patent No. 6423829
; GENERAL INFORMATION:
; APPLICANT: Belt, Judith A.
; APPLICANT: Crawford, Charles R.
; APPLICANT: Patel, Divyen
; TITLE OF INVENTION: A NITROBENZYLMECAPTOPURINERIBOSIDE
; TITLE OF INVENTION: (NEMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
; TITLE OF INVENTION: PROTEIN, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
; TITLE OF INVENTION: USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/611,781
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/058,389
; FILING DATE: April 9, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.

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OM nucleic - nucleic search, using sw model

Run on: November 5, 2004, 20:38:03 ; Search time 376 Seconds
(without alignments)

7059.492 Million cell updates/sec

Title: US-09-882-434A-2

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Searched: 3611042 seqs, 2692057975 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
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19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
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21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*
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SUMMARIES

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c	39.6	8.0	632	18	Sequence 2, Appli
3	35.6	7.2	516	13	Sequence 66398, A
4	35.6	7.2	516	15	US-10-027-632-272863
c	35.6	7.2	8011	15	Sequence 272863,
6	35.4	7.2	2035	15	Sequence 51, Appl
7	35.4	7.2	2035	16	Sequence 1814, Ap
8	35.4	7.2	2658	14	US-10-198-846-10674
9	35.4	7.2	3043	15	US-10-104-047-374
10	35.2	7.1	6375	15	US-10-311-455-1997
11	35.2	7.1	39342	16	Sequence 1997, Ap
c	34.8	7.1	179	10	Sequence 471, App
					Sequence 43, Appl

13	34.4	7.0	516	13	US-10-027-632-272862	Sequence 272862,	
14	34.4	7.0	516	15	US-10-027-632-272862	Sequence 272862,	
c	15	2000	16	US-10-260-238-2032	Sequence 2032, Ap	Sequence 2032, Ap	
16	34.4	7.0	82293	16	US-10-433-580-1	Sequence 1, Appl	
c	17	34.2	431	14	US-10-208-408-43	Sequence 43, Appl	
c	18	34	6.9	7005	15	US-10-369-493-26248	Sequence 26248, Ap
c	19	33.8	481	16	US-10-240-425-1382	Sequence 1382, Ap	
c	20	33.8	6.9	367378	15	US-10-312-841-2	Sequence 2, Appl
21	33.6	6.8	729	13	US-10-027-632-151539	Sequence 151539,	
22	33.6	6.8	729	15	US-10-027-632-151539	Sequence 151539,	
23	33.6	6.8	2000	16	US-10-260-238-1988	Sequence 1988, Ap	
24	33.6	6.8	3493	13	US-10-027-632-112760	Sequence 112760,	
25	33.6	6.8	3493	15	US-10-027-632-112760	Sequence 112760,	
c	26	33.4	777	17	US-10-415-478A-35	Sequence 35, Appl	
c	27	33.4	6.8	9223	8	US-08-961-527-59	Sequence 59, Appl
c	28	33.4	6.8	9223	16	US-10-158-844-59	Sequence 59, Appl
c	29	33.4	6.8	27540	17	US-10-415-478A-10	Sequence 10, Appl
c	30	33.2	6.7	139389	15	US-10-236-031B-61	Sequence 61, Appl
c	31	33	6.7	62909	16	US-10-672-787-32	Sequence 32, Appl
32	32.8	6.7	1324	16	US-10-424-599-121388	Sequence 121388,	
c	33	32.8	6.7	5497	15	US-10-311-455-710	Sequence 710, App
c	34	32.8	6.7	13784	16	US-10-257-166-143	Sequence 143, App
c	35	32.8	6.7	21814	17	US-10-316-540-4	Sequence 4, Appl
c	36	32.6	6.6	364	16	US-10-424-599-93607	Sequence 93607, A
37	32.6	6.6	17142	14	US-10-239-676-206	Sequence 206, App	
38	32.6	6.6	17142	15	US-10-311-455-2080	Sequence 2080, Ap	
39	32.6	6.6	17142	15	US-10-240-453-304	Sequence 304, App	
40	32.4	6.6	463	9	US-09-864-761-6488	Sequence 6488, App	
41	32.4	6.6	478	13	US-10-027-632-186833	Sequence 186833,	
42	32.4	6.6	478	15	US-10-027-632-186833	Sequence 186833,	
43	32.4	6.6	1170	13	US-10-027-632-123172	Sequence 123172,	
44	32.4	6.6	1170	15	US-10-027-632-123172	Sequence 123172,	
c	45	32.4	1269	16	US-10-282-122A-40614	Sequence 40614, A	

ALIGNMENTS

RESULT 1

US-09-882-434A-2
; Sequence 2, Application US/09882434A
; Patent No. US20020108144A1
; GENERAL INFORMATION:
; APPLICANT: Manners, John M.
; APPLICANT: Marcus, John Paul
; APPLICANT: Goulter, Kenneth C.
; APPLICANT: Green, Jodie Lyn
; TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
; FILE REFERENCE: CULLN18.1CPI1
; CURRENT APPLICATION NUMBER: US/09/882,434A
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/364395
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/117615
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/AU97/00052
; PRIOR FILING DATE: 1997-01-31
; PRIOR APPLICATION NUMBER: AU PN 7802
; PRIOR FILING DATE: 1996-01-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 493
; TYPE: DNA
; ORGANISM: Macadamia integrifolia
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (70)...(375)
; OTHER INFORMATION: y=t or c.
US-09-882-434A-2

Query Match 99.9% Score 492.6; DB 9; Length 493;
Best Local Similarity 100.0%; Pred. No. 1e-140;


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; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 272863
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-272863

Query Match 7.2%; Score 35.6; DB 15; Length 516;
Best Local Similarity 50.6%; Pred. No. 3.3;
Matches 83; Conservative 1; Mismatches 80; Indels 0; Gaps 0;

.QY 292 TGCAGTGGTGTGCACACACAGGTTGGTCCAGTCCAGGCGCATGCCAACCCCTTTTGGT 351
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
318 TTCAGATCAGTTGCAGCAAGAGTTAAGCATAGAGTCTCGGAGTTAGACTGCTGGGTC 377
QY 352 TGGAGAGTAGTCTTCATCCATGCTAGATTTTCATACCTCTTGGATCCATCTTCTATGTTT 411
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
378 TCAAGCATAGCTCCATCAGTTACTAGATGTGTAACCTTGGTTATGAGCATCTAATGATC 437
QY 412 TTCAAGTGTATAATTAGAGAGATGCATGATATATAATAATAA 455
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
438 GTCAGTTTCATCAGTGAATGACAGTAATAATAATAACTGA 481

RESULT 5
US-10-311-455-51/c
; Sequence 51, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 51
; LENGTH: 8011
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; US-10-311-455-51

Query Match 7.2%; Score 35.6; DB 15; Length 8011;
Best Local Similarity 58.5%; Pred. No. 14;
Matches 62; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 361 ATCTTCATCCATGCTAGATTTCAATCTTTGGATCCATCTTCTATGTTTTCAGAGTGT 420
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3147 ATCTAAATTTAACCAATCTACCTAAATCCAAACCATCTTTTAACTTTTCAATATA 3088
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QY 421 ATAAATTAGAGATGCGATGATATATAATAAATAAGTAAAGCTAC 466
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3087 TTACATAATTACATACAAACAAATAATAATAATAAAAAAACC 3042

RESULT 6
US-10-172-118-1814
; Sequence 1814, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1814
; LENGTH: 2035
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_019049
; DATABASE ENTRY DATE: 2001-06-18
; US-10-172-118-1814

Query Match 7.2%; Score 35.4; DB 15; Length 2035;
Best Local Similarity 55.2%; Pred. No. 7.9;
Matches 69; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 345 TTTTGGTTGGAAGAGTATCTTCATCCATGCGATGATTCATTAATAGTAAAGCT 404
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1269 TATTTGAGGAATGCGCAACTCATATATTTTTCATTTGCAATTCACACATTTTC 1328
QY 405 TATGTTTTTCAAGTGATATATAGAGAGATGCGATGATATATAATAAGTAAAGCT 464
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1329 TCACCTGTTTCATTTGAGGATATATGAATGATGATTTTAAATATAAGCGAATCT 1388
QY 465 ACGGT 469
Db |||||
1389 ACTGT 1393

RESULT 7
US-10-342-887-1814
; Sequence 1814, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
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; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1814
; LENGTH: 2035
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1814

Query Match          7.2%; Score 35.4; DB 16; Length 2035;
Best Local Similarity 55.2%; Pred. No. 7.9;
Matches 69; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 345 TTTTGGTTGGAAGAGTATCTTCATCCAAATGCTAGATTTTCATAACTCTTGGATCCATCTTC 404
Db 1269 TATTGTGAGAAATGGCAACTCACTACTATTAAATTTTTTTTGCATTGCAACATTTTTC 1328

QY 405 TATGTTTTTCAAGTGTATAATTAGAGAGATGCGATGATATATAATAAATAGTAAAGCT 464
Db 1329 TCACCTTTTCATTTCGAGGATATATGAAATGCAATGATTTTAAATATAAAGCGAATTCT 1388

QY 465 ACGGT 469
Db 1389 ACTGT 1393

RESULT 8
US-10-198-846-10674
; Sequence 10674, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steimann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: THERAPY OF BREAST CANCER
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10674
; LENGTH: 2658
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2650,
; LOCATION: 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-10674

Query Match          7.2%; Score 35.4; DB 14; Length 2658;
Best Local Similarity 55.2%; Pred. No. 9.1;
Matches 69; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 345 TTTTGGTTGGAAGAGTATCTTCATCCAAATGCTAGATTTTCATAACTCTTGGATCCATCTTC 404
Db 1891 TATTGTGAGAAATGGCAACTCACTACTATTAAATTTTTTTTGCATTGCAACATTTTTC 1950

QY 405 TATGTTTTTCAAGTGTATAATTAGAGAGATGCGATGATATATAATAAATAGTAAAGCT 464
Db 1951 TCACCTTTTCATTTCGAGGATATATGAAATGCAATGATTTTAAATATAAAGCGAATTCT 2010

QY 465 ACGGT 469
Db 2011 ACTGT 2015

RESULT 9

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FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 272862
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-272862
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Query Match      7.0%; Score 34.4; DB 15; Length 516;
Best Local Similarity 50.6%; Pred. No. 7.7;
Matches 83; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 292 TGCAGTGGTGTGGACACACAGAGTTTGGGTCCAGTGCAGGGGATGCAACCCCTTTTGGT 351
Db 318 TTCAGATCAGTTGCGAGCAAGATTAGCATAGAGTCTCTGGAGTTAGACTGCTGGGTC 377

QY 352 TGGAGAGATATCTTCATCCAAATGCTAGATTTCATAACTCTCTGGATCCATCTTCTATGTTT 411
Db 378 TCAAGCCATAGTCCATCAGTTACTAGATGTGTACCTTTGGTTATGAGCATCTATGTAC 437

QY 412 TTCAAGTGTATAATTAGAGAGATGCATGCGATATATAATAA 455
Db 438 GTCAGTTTCTTCATCAGTGAATGACAGTAATAATAAATCTGA 481
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RESULT 15
US-10-260-238-2032/c
; Sequence 2032, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 2032
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Oryza sativa
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US-10-260-238-2032
Query Match      7.0%; Score 34.4; DB 16; Length 2000;
Best Local Similarity 65.8%; Pred. No. 16;
Matches 50; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 390 CTTGGATCCATCTTCTATGTCTTTTCAAGTGTATATTAATTAGAGAGATGCATGATATAAT 449
Db 1389 CTTAATTTCACTACAAATGTTTCCATTAGAGATTAAGAAATGCTTGGATGGATCAT 1330

QY 450 AAATAAGTAAAGCTA 465
Db 1329 CAATCAATAATAACCA 1314
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Search completed: November 5, 2004, 21:55:39
Job time : 382 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 5, 2004, 21:49:14 ; Search time 102 Seconds
(without alignments)
353.226 Million cell updates/sec

Title: US-09-882-434A-1

Perfect score: 551

Sequence: 1 MASTKLFPSVITVWMLIAMA.....FGSSARACNPFQWKSIFIQC 102

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1566620 seqs, 353225886 residues

Total number of hits satisfying chosen parameters: 1566620

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	551	100.0	102	9	US-09-882-434A-1
2	426	77.3	76	9	US-09-882-434A-15
3	426	77.3	76	9	US-09-882-434A-16
4	426	77.3	76	9	US-09-882-434A-17
5	421	76.4	76	9	US-09-882-434A-19
6	419	76.0	76	9	US-09-882-434A-18
7	417	75.7	76	9	US-09-882-434A-21
8	415	75.3	76	9	US-09-882-434A-20
9	183	33.2	116	17	US-10-425-115-251061
10	80.5	14.6	500	15	US-10-424-599-214772
11	75.5	13.7	486	9	US-09-801-368-154
12	75.5	13.7	486	14	US-10-369-493-21896
13	73.5	13.3	232	15	US-10-424-599-179163

14	73	13.2	92	16	US-10-437-963-184834
15	72	13.1	507	14	US-10-156-761-10129
16	71.5	13.0	403	15	US-10-282-122A-55057
17	71	12.9	68	17	US-10-425-115-303206
18	71	12.9	235	17	US-10-739-930-10191
19	71	12.9	1280	14	US-10-101-433A-3
20	71	12.9	1280	15	US-10-619-359A-2
21	71	12.9	1283	14	US-10-101-433A-2
22	71	12.9	1283	14	US-10-101-433A-4
23	71	12.9	1283	15	US-10-619-359A-4
24	70.5	12.8	267	9	US-09-764-868-1164
25	70.5	12.8	267	10	US-09-764-891-4089
26	70	12.7	167	16	US-10-437-963-151301
27	69	12.7	1280	13	US-10-044-671-2
28	69	12.5	1280	14	US-10-101-433A-11
29	69	12.5	1280	15	US-10-619-359A-7
30	69	12.5	1281	14	US-10-101-433A-7
31	69	12.5	1281	14	US-10-101-433A-8
32	69	12.5	1281	14	US-10-101-433A-9
33	69	12.5	1281	14	US-10-101-433A-10
34	68.5	12.4	78	14	US-10-178-213-431
35	68.5	12.4	1557	14	US-10-369-493-6816
36	68.5	12.4	1887	10	US-09-853-180-3
37	68	12.3	174	15	US-10-424-599-253845
38	68	12.3	461	14	US-10-081-872-82
39	68	12.3	461	14	US-10-105-733-10
40	68	12.3	461	14	US-10-081-739A-10
41	68	12.3	461	15	US-10-385-305-82
42	68	12.3	579	9	US-09-805-020-67
43	68	12.3	1278	9	US-09-805-020-66
44	68	12.3	1280	9	US-09-817-762-3
45	68	12.3	1280	9	US-09-866-866A-2

ALIGNMENTS

RESULT 1

US-09-882-434A-1
; Sequence 1, Application US/09882434A
; Patent No. US20020108144A1
; GENERAL INFORMATION:
; APPLICANT: Manners, John M.
; APPLICANT: Marcus, John Paul
; APPLICANT: Goulter, Kenneth C.
; APPLICANT: Green, Jodie Lyn
; TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
; FILE REFERENCE: CULN18.1CPI1
; CURRENT APPLICATION NUMBER: US/09/882,434A
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/364395
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/117615
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/AU97/00052
; PRIOR FILING DATE: 1997-01-31
; PRIOR APPLICATION NUMBER: AU PN 7802
; PRIOR FILING DATE: 1996-01-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Macadamia integrifolia
US-09-882-434A-1

Query Match 100.0%; Score 551; DB 9; Length 102;
Best Local Similarity 100.0%; Pred. No. 7.5e-56;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTKLFPSVITVWMLIAMASEMVNGSAFTVWSPGNNRAERYSKGCSAIHQGGYDF 60
DB 1 MASTKLFPSVITVWMLIAMASEMVNGSAFTVWSPGNNRAERYSKGCSAIHQGGYDF 60

```
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mi39K variant. Variant MIAMP1 protein Mi39K
; OTHER INFORMATION: containing a Lysine at amino acid 39 (used primer
; OTHER INFORMATION: from SEQ ID NO:9 to produce).
US-09-882-434A-16

Query Match          77.3%; Score 426; DB 9; Length 76;
Best Local Similarity 98.7%; Pred. No. 1.6e-41;
Matches 75; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 SAFTWSGPGCNCNRAERYSKGCSAIHQKGGYDFSVTGTTAALYNQAGCGVAHTRFGSS 86
Db 1 SAFTWSGPGCNCNRAERYSKGCSAIHQKGGYDFSVTGTTAALYNQAGCGVAHTRFGSS 60

QY 87 ARACNPFGWKSIFIOC 102
Db 61 ARACNPFGWKSIFIOC 76

RESULT 4
US-09-882-434A-17
; Sequence 17, Application US/09882434A
; Patent No. US20020108144A1
; GENERAL INFORMATION:
; APPLICANT: Manners, John M.
; APPLICANT: Marcus, John Paul
; APPLICANT: Goulter, Kenneth C.
; APPLICANT: Green, Jodie Lyn
; TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
; FILE REFERENCE: CULLN18.1CPI1
; CURRENT APPLICATION NUMBER: US/09/882.434A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/364395
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/117615
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/AU97/00052
; PRIOR FILING DATE: 1997-01-31
; PRIOR APPLICATION NUMBER: AU PN 7802
; PRIOR FILING DATE: 1996-01-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mi46K variant. Variant MIAMP1 protein Mi46K
; OTHER INFORMATION: containing a Lysine at amino acid 46 (used primer
; OTHER INFORMATION: from SEQ ID NO:10 to produce).
US-09-882-434A-17

Query Match          77.3%; Score 426; DB 9; Length 76;
Best Local Similarity 98.7%; Pred. No. 1.6e-41;
Matches 75; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 SAFTWSGPGCNCNRAERYSKGCSAIHQKGGYDFSVTGTTAALYNQAGCGVAHTRFGSS 86
Db 1 SAFTWSGPGCNCNRAERYSKGCSAIHQKGGYDFSVTGTTAALYNQAGCGVAHTRFGSS 60

QY 87 ARACNPFGWKSIFIOC 102
Db 61 ARACNPFGWKSIFIOC 76

RESULT 5
US-09-882-434A-19
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QY 61 SYTGQTAAALYNQAGCGVAHTRFGSSARACNPFGWKSIFIOC 102
Db 61 SYTGQTAAALYNQAGCGVAHTRFGSSARACNPFGWKSIFIOC 102

RESULT 2
US-09-882-434A-15
; Sequence 15, Application US/09882434A
; Patent No. US20020108144A1
; GENERAL INFORMATION:
; APPLICANT: Manners, John M.
; APPLICANT: Marcus, John Paul
; APPLICANT: Goulter, Kenneth C.
; APPLICANT: Green, Jodie Lyn
; TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
; FILE REFERENCE: CULLN18.1CPI1
; CURRENT APPLICATION NUMBER: US/09/882.434A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/364395
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/117615
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/AU97/00052
; PRIOR FILING DATE: 1997-01-31
; PRIOR APPLICATION NUMBER: AU PN 7802
; PRIOR FILING DATE: 1996-01-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mi28K variant. Variant MIAMP1 protein Mi28K
; OTHER INFORMATION: containing a Lysine at amino acid 28 (used primer
; OTHER INFORMATION: from SEQ ID NO:8 to produce).
US-09-882-434A-15

Query Match          77.3%; Score 426; DB 9; Length 76;
Best Local Similarity 98.7%; Pred. No. 1.6e-41;
Matches 75; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 SAFTWSGPGCNCNRAERYSKGCSAIHQKGGYDFSVTGTTAALYNQAGCGVAHTRFGSS 86
Db 1 SAFTWSGPGCNCNRAERYSKGCSAIHQKGGYDFSVTGTTAALYNQAGCGVAHTRFGSS 60

QY 87 ARACNPFGWKSIFIOC 102
Db 61 ARACNPFGWKSIFIOC 76

RESULT 3
US-09-882-434A-16
; Sequence 16, Application US/09882434A
; Patent No. US20020108144A1
; GENERAL INFORMATION:
; APPLICANT: Manners, John M.
; APPLICANT: Marcus, John Paul
; APPLICANT: Goulter, Kenneth C.
; APPLICANT: Green, Jodie Lyn
; TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
; FILE REFERENCE: CULLN18.1CPI1
; CURRENT APPLICATION NUMBER: US/09/882.434A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/364395
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/117615
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/AU97/00052
; PRIOR FILING DATE: 1997-01-31
; PRIOR APPLICATION NUMBER: AU PN 7802
; PRIOR FILING DATE: 1996-01-31
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; Sequence 19, Application US/09882434A
; Patent No. US20020108144A1
; GENERAL INFORMATION:
; APPLICANT: Manners, John M.
; APPLICANT: Marcus, John Paul
; APPLICANT: Goulter, Kenneth C.
; APPLICANT: Green, Jodie Lyn
; TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
; FILE REFERENCE: CULLN18.1CPI1
; CURRENT APPLICATION NUMBER: US/09/882.434A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/364395
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/117615
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/AU97/00052
; PRIOR FILING DATE: 1997-01-31
; PRIOR APPLICATION NUMBER: AU PN 7802
; PRIOR FILING DATE: 1996-01-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: M154K variant. Variant MiAMP1 protein M154K
; OTHER INFORMATION: containing a Lysine at amino acid 54 (used primer
; OTHER INFORMATION: from SEQ ID NO:12 to produce).
US-09-882-434A-19

Query Match          76.4%; Score 421; DB 9; Length 76;
Best Local Similarity 98.7%; Pred. No. 6.1e-41;
Matches 75; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 27 SAFTVWSGPGCNRAERYSKGCSAIHQKGYDFSITGQTAAALYNQACSGVAHTRFGSS 86
Db 1 SAFTVWSGPGCNRAERYSKGCSAIHQKGYDFSITGQTAAALYNQACSGVAHTRFGSS 60

Qy 87 ARACNPFGWKSIFIQ 102
Db 61 ARACNPFGWKSIFIQ 76

RESULT 6
US-09-882-434A-18
; Sequence 18, Application US/09882434A
; Patent No. US20020108144A1
; GENERAL INFORMATION:
; APPLICANT: Manners, John M.
; APPLICANT: Marcus, John Paul
; APPLICANT: Goulter, Kenneth C.
; APPLICANT: Green, Jodie Lyn
; TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
; FILE REFERENCE: CULLN18.1CPI1
; CURRENT APPLICATION NUMBER: US/09/882.434A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/364395
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/117615
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/AU97/00052
; PRIOR FILING DATE: 1997-01-31
; PRIOR APPLICATION NUMBER: AU PN 7802
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: M154V variant. Variant MiAMP1 protein M154V
; OTHER INFORMATION: containing a Lysine at amino acid 54 (used primer
; OTHER INFORMATION: from SEQ ID NO:11 to produce).
US-09-882-434A-18

Query Match          75.7%; Score 417; DB 9; Length 76;
Best Local Similarity 97.4%; Pred. No. 1.8e-40;
Matches 74; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 27 SAFTVWSGPGCNRAERYSKGCSAIHQKGYDFSITGQTAAALYNQACSGVAHTRFGSS 86
Db 1 SAFTVWSGPGCNRAERYSKGCSAIHQKGYDFSITGQTAAALYNQACSGVAHTRFGSS 60

Qy 87 ARACNPFGWKSIFIQ 102
Db 61 ARACNPFGWKSIFIQ 76

RESULT 7
US-09-882-434A-21
; Sequence 21, Application US/09882434A
; Patent No. US20020108144A1
; GENERAL INFORMATION:
; APPLICANT: Manners, John M.
; APPLICANT: Marcus, John Paul
; APPLICANT: Goulter, Kenneth C.
; APPLICANT: Green, Jodie Lyn
; TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
; FILE REFERENCE: CULLN18.1CPI1
; CURRENT APPLICATION NUMBER: US/09/882.434A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/364395
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/117615
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/AU97/00052
; PRIOR FILING DATE: 1997-01-31
; PRIOR APPLICATION NUMBER: AU PN 7802
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: M146K/54K variant. Variant MiAMP1 protein
; OTHER INFORMATION: M146K/54K containing a Lysine at amino acid 46 and
; OTHER INFORMATION: a Lysine at amino acid 54.
US-09-882-434A-21

Query Match          75.7%; Score 417; DB 9; Length 76;
Best Local Similarity 97.4%; Pred. No. 1.8e-40;
Matches 74; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 27 SAFTVWSGPGCNRAERYSKGCSAIHQKGYDFSITGQTAAALYNQACSGVAHTRFGSS 86
Db 1 SAFTVWSGPGCNRAERYSKGCSAIHQKGYDFSITGQTAAALYNQACSGVAHTRFGSS 60

Qy 87 ARACNPFGWKSIFIQ 102
Db 61 ARACNPFGWKSIFIQ 76

RESULT 8
US-09-882-434A-20
; Sequence 20, Application US/09882434A
; Patent No. US20020108144A1
; GENERAL INFORMATION:
; APPLICANT: Manners, John M.
; APPLICANT: Marcus, John Paul
; APPLICANT: Goulter, Kenneth C.
; APPLICANT: Green, Jodie Lyn
; TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
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; FILE REFERENCE: CULLN18.1CPI.C1
; CURRENT APPLICATION NUMBER: US/09/882.434A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/364395
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/117615
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/AU97/00052
; PRIOR FILING DATE: 1997-01-31
; PRIOR APPLICATION NUMBER: AU PN 7802
; PRIOR FILING DATE: 1996-01-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: M146K/54V variant. Variant M1AMP1 protein
; OTHER INFORMATION: M146K/54V containing a Lysine at amino acid 46 and
; OTHER INFORMATION: a Valine at amino acid 54.
US-09-882-434A-20

Query Match 75.3%; Score 415; DB 9; Length 76;
Best Local Similarity 97.4%; Pred. No. 3e-40; 1; Indels 0; Gaps 0;
Matches 74; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 27 SAFTWSPGNCNRAERYSKGCSAIHOKGGYDFSYTGQTAALYNQAGCSGVVHTRFGSS 86
Db 1 SAFTWSPGNCNRAERYSKGCSAIHOKGGYDFSYTGQTAALYNKAGCSGVVHTRFGSS 60

QY 87 ARACNPPGKWSIFIQC 102
Db 61 ARACNPPGKWSIFIQC 76

RESULT 9
US-10-425-115-251061
; Sequence 251061, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 251061
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_160554C.1.pep
US-10-425-115-251061

Query Match 33.2%; Score 183; DB 17; Length 116;
Best Local Similarity 36.1%; Pred. No. 3.5e-13;
Matches 43; Conservative 17; Mismatches 39; Indels 20; Gaps 5;

QY 1 MASTK---LFFSVITVMMLIA-----MASEMVNGSAFTVWSPGNCNRAERY--- 44
Db 1 MASTKAATMF--VATAVAIAATVAAATGWASDCGSPRSYLTWSGGPGCTTGKGHAS 58

QY 45 -SKCGSAIHOKGYDFSYTGQTAALYNQAGCSGVVHTRFGSSARACNPPGKWSIFIQC 102
Db 59 AGSCGCNHLRFHGHGFNFRGTATLYSQPCVGTPIQVF-EDTQACGDFGWSHIIDC 116

RESULT 10
US-10-424-599-214772
; Sequence 214772, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 214772
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(500)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_35966C.1.pep
US-10-424-599-214772

Query Match 14.6%; Score 80.5; DB 15; Length 500;
Best Local Similarity 29.3%; Pred. No. 1.3; 19; Indels 31; Gaps 7;
Matches 24; Conservative 8; Mismatches 19; Indels 31; Gaps 7;

QY 34 GPGCNRAERYSKGCSAIHOKGG-----YDFSYTGQTAALYNQAGCS-----GVAHTR 82
Db 145 GSGCEG-----GCRVVHASNGVRRSAIEFGH-----LHSHA-CSCFGVXCGIKSKR 189

QY 83 FGSSARACNPPGKW--SIFIQC 102
Db 190 FG---KICKPLTWKHGDIPLMC 208

RESULT 11
US-09-801-368-154
; Sequence 154, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
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; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 154
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-154
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; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10129
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10129

Query Match      13.1%; Score 72; DB 14; Length 507;
Best Local Similarity 24.3%; Pred. No. 13;
Matches 25; Conservative 19; Mismatches 43; Indels 16; Gaps 3;

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Db      390 IVQSEIFGVLVLLPFDSDDEGIRLANDTPYGLAASAMSRDVIYRANRATREIKAGCYWVN 449
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Qy      54 Q-----KGYDFSVYTGQTALYNOAGCGVAHTRFGSSA 87
Db      450 DHIPIISEMPHGGYKASGFGKMSAYSFEYTKIKHVMFDNTA 492
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